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Sequence Listing could not be accepted.

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Reviewer: markspencer

Timestamp: Thu May 24 14:13:01 EDT 2007

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Reviewer Comments:

<210> 1

<211> 1629

<212> DNA

<213> Unknown

<220>

<223> Environmental

The use of "Environmental", for numeric identifier <223>, is insufficient. Please

explain the source of the genetic material. When Unknown is used for the organism.

The source can be a broad category such as Mammalian, Bacterial, Viral...etc.

Note, several sequences need this change.

Application No: 10576122 Version No: 1.0

Input Set:

Output Set:

Started: 2007-05-23 23:04:23.095
Finished: 2007-05-23 23:04:23.508
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 413 ms
Total Warnings: 3
Total Errors: 0
No. of SeqIDs Defined: 6
Actual SeqID Count: 6

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)

SEQUENCE LISTING

<110> MORGAN, Brian
BURK, Mark
LEVIN, Michael
ZHU, Zoulin
CHAPLIN, Jennifer
KUSTEDJO, Karen
HUANG, Zilin
GREENBERG, William

<120> METHODS FOR MAKING SIMVASTATIN AND INTERMEDIATES

<130> 564462012800

<140> 10576122
<141> 2007-05-23

<150> US 10/576,122
<151> 2004-10-20

<150> PCT/US2004/034913
<151> 2004-10-20

<150> US 60/542,100
<151> 2004-02-04

<150> US 60/513,237
<151> 2003-10-21

<160> 6

<170> PatentIn version 3.1

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Gly Leu Glu Leu Pro Tyr Thr Thr Ile Thr Ser Ala Ala Val Ala Thr
35 40 45

Glu Gly Pro Ile Pro Gln Pro Ala Ile Phe Gly Ser Thr Asp Pro Ile
50 55 60

Val Ala Pro Glu Arg Cys Glu Val Arg Ala Val Thr Arg Pro Thr Lys
65 70 75 80

Asp Ser Glu Ile Arg Ile Glu Leu Trp Leu Pro Leu Ser Gly Trp Asn
85 90 95

Gly Lys Tyr Leu Gln Ile Gly Ser Gly Gly Trp Ala Gly Ser Ile Asn
100 105 110

Arg Thr Gly Leu Ile Gly Pro Leu Gln Arg Gly Tyr Ala Val Ala Ala
115 120 125

Thr Asp Asn Gly His Ile Ser Glu Gly Leu Val Pro Asp Ala Ser Trp
130 135 140

Ala Ile Gly His Pro Gln Lys Leu Ile Asp Phe Gly Tyr Arg Ala Val
145 150 155 160

His Glu Thr Ser Val Gln Ala Lys Ala Ile Leu Arg Ala Tyr Phe Gly
165 170 175

Arg Gly Gln Asp Leu Ser Tyr Phe Ser Gly Cys Ser Asn Gly Gly Arg
180 185 190

Glu Ala Leu Met Glu Ala Gln Arg Tyr Pro Glu Asp Phe Glu Gly Ile
195 200 205

Ile Ala Gly Ala Pro Ala Asn Asn Trp Ser Arg Leu Phe Thr Gly Phe
210 215 220

Val Trp Asn Glu Arg Ala Leu Ala Asp Asp Pro Ile Pro Pro Ala Lys
225 230 235 240

Leu Thr Ala Ile Gln Ala Ala Ala Ile Ala Ala Cys Asp Thr Leu Asp
245 250 255

Gly Val Glu Asp Gly Leu Ile Glu Asn Pro Arg Ala Cys Ser Phe Asp
260 265 270

Pro Arg Ser Met Val Cys Thr Ala Asp Asp Ala Ser Asp Cys Leu Thr
275 280 285

Glu Gly Gln Val Ala Thr Leu His Arg Ile Tyr Ser Gly Pro Thr Asn
290 295 300

Pro Arg Thr Gly Glu Arg Ile Phe Pro Gly Tyr Pro Met Gly Thr Glu
305 310 315 320

Ala Val Pro Gly Gly Trp Val Pro Trp Ile Val Ser Ala Ser Ser Glu
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Val Pro Ser Ile Gln Ala Ser Phe Gly Asn Ser Tyr Tyr Gly His Ala
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Val Phe Glu Gln Ser Asn Trp Asp Phe Arg Thr Leu Asp Phe Asp Gln
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Asp Val Ala Phe Gly Asp Ala Lys Ala Gly Pro Val Leu Asn Ala Thr
370 375 380

Asn Pro Asp Leu Arg Ser Phe Arg Ala Asn Gly Gly Lys Leu Ile Gln
385 390 395 400

Tyr His Gly Trp Gly Asp Ala Ala Ile Thr Ala Phe Ser Ser Ile Asp
405 410 415

Tyr Tyr Glu Asn Val Arg Ala Phe Leu Asp Arg Phe Pro Asp Pro Arg
420 425 430

Ser Glu Asn Thr Asp Ile Asp Gly Phe Tyr Arg Leu Phe Leu Val Pro
435 440 445

Gly Met Gly His Cys Ser Gly Gly Ile Gly Pro Ser Ser Phe Gly Asn
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Gly Phe Arg Ser Ala Arg Thr Asp Ala Glu His Asp Leu Leu Ser Ala

465 470 475 480

Leu Glu Ala Trp Val Glu Arg Asp Thr Ala Pro Glu Arg Leu Ile Gly

485 490 495

Thr Gly Thr Ala Val Gly Asp Pro Thr Ala Thr Leu Thr Arg Pro Leu

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Cys Pro Tyr Pro Arg Thr Ala Arg Tyr Leu Gly Ser Gly Asn Ser Asn

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Asp Ala Ala Asn Phe Glu Cys Ala Leu Pro Ala Gly Val Gln

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<211> 1209

<212> DNA

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<220>

<223> Environmental

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gtagtgact tggggggcgcatggcgcatg gcccacactc agacgcccattg gacggcgagg 180

acggtcagta ttgttttttc ctccaccaaa ggcgcaacgg cactctgcgc ccatatgtg 240

gcgtcacgcg gccaactgga tcttgcgtca ccagtcgcca cctactggcc ggaatttgc 300

caagccggca aagctcgcat cccgggtgaaa atgctttga accatcaagc tggctccct 360

gccgtacgga caccgctgcc ccagggtgcc tacgctgact gggactgtat ggtcaatacg 420

ttggccaagg aagagccgtt ttgggaacct ggcacccgca acggctatca tgcgttcacc 480

atggggtgcc tgggtggaga agtggtgccgat cgtgtctctg gtaagtcgct tgggacattc 540

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<212> PRT

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Cys Val Thr Leu His Gly Glu Thr Val Val Asp Leu Trp Gly Gly Met
 35 40 45

Ala Arg Ala Asp Thr Gln Thr Pro Trp Thr Ala Glu Thr Val Ser Ile
50 55 60

Val Phe Ser Ser Thr Lys Gly Ala Thr Ala Leu Cys Ala His Met Leu
65 70 75 80

Ala Ser Arg Gly Gln Leu Asp Leu Asp Ala Pro Val Ala Thr Tyr Trp
85 90 95

Pro Glu Phe Ala Gln Ala Gly Lys Ala Arg Ile Pro Val Lys Met Leu
100 105 110

Leu Asn His Gln Ala Gly Leu Pro Ala Val Arg Thr Pro Leu Pro Gln
115 120 125

Gly Ala Tyr Ala Asp Trp Glu Leu Met Val Asn Thr Leu Ala Lys Glu
130 135 140

Glu Pro Phe Trp Glu Pro Gly Thr Arg Asn Gly Tyr His Ala Leu Thr
145 150 155 160

Met Gly Trp Leu Val Gly Glu Val Val Arg Arg Val Ser Gly Lys Ser
165 170 175

Leu Gly Thr Phe Phe Gln Glu Glu Ile Ala Arg Pro Leu Gly Leu Asp
180 185 190

Phe Trp Ile Gly Leu Pro Ala Glu Gln Glu Ala Arg Val Ala Pro Met
195 200 205

Ile Ala Ala Glu Pro Asp Pro Gln Ser Leu Phe Phe Gln Glu Val Ala
210 215 220

Lys Pro Gly Ala Leu Gln Ser Leu Val Leu Leu Asn Ser Gly Gly Tyr
225 230 235 240

Met Gly Ala Gln Pro Glu Tyr Asp Ser Arg Ala Ala His Ala Ala Glu
245 250 255

Ile Gly Ala Ala Gly Gly Ile Thr Asn Ala Arg Gly Leu Ala Gly Met
260 265 270

Tyr Ala Pro Leu Ala Cys Gly Gly Lys Leu Lys Gly Val Glu Leu Val
275 280 285

Ser Pro Asp Met Leu Ala Arg Met Ser Arg Val Ala Ser Ala Thr Gly
290 295 300

Arg Asp Ala Val Leu Met Met Pro Thr Arg Phe Ala Leu Gly Phe Met
305 310 315 320

Lys Ser Met Asp Asn Arg Arg Glu Pro Ala Gly Val Gln Asp Ser Ala
325 330 335

Leu Phe Gly Glu Glu Ala Phe Gly His Val Gly Ala Gly Gly Ser Phe
340 345 350

Gly Phe Ala Asp Pro Lys Ala Gly Met Ser Phe Gly Tyr Thr Met Asn
355 360 365

Arg Met Gly Leu Gly Ala Gly Leu Asn Pro Arg Gly Gln Ser Leu Val
370 375 380

Asp Ala Thr Tyr Arg Ser Leu Gly Tyr Gln Ser Asp Ala Ser Gly Ala
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Trp Thr

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<211> 1578

<212> DNA

<213> Unknown

<220>

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cttcccaaca cgacgatcac ctcggcccaag accgtcacca ccggatcggtt aacgcccccg 180

ggctcgacga atccgatcac cgacctgcct cctttctgcc gtgtcacagg cgccatcgcc 240

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aagttcgccg gcgtgggcaa cggcggtgg gccggcatca tctccttcgg cgccctcgga 360

agccagctca agcgcggcta cgcgaccgccc tccacgaata cgggtcacga agcggcgccg 420

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gccccaaacgt ttccggccga ctacgacggg atcgtcgccg gtatgccggc gaacaactgg 660

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<213> Unknown

<220>

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35															

Ala	Gln	Thr	Val	Thr	Thr	Gly	Ser	Leu	Thr	Pro	Pro	Gly	Ser	Thr	Asn
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65

70

75

80

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85 90 95

Lys Trp Asn Gly Lys Phe Ala Gly Val Gly Asn Gly Gly Trp Ala Gly
100 105 110

Ile Ile Ser Phe Gly Ala Leu Gly Ser Gln Leu Lys Arg Gly Tyr Ala
115 120 125

Thr Ala Ser Thr Asn Thr Gly His Glu Ala Ala Pro Gly Met Asn Ala
130 135 140

Ala Arg Phe Ala Phe Glu Lys Pro Glu Gln Leu Ile Asp Phe Ala Tyr
145 150 155 160

Arg Ser Gln His Glu Thr Ala Leu Lys Ala Lys Ala Leu Val Gln Ala
165 170 175

Phe Tyr Gly Lys Pro Pro Glu His Ser Tyr Phe Ile Gly Cys Ser Ser
180 185 190

Gly Gly Tyr Gln Gly Leu Met Glu Ala Gln Arg Phe Pro Ala Asp Tyr
195 200 205

Asp Gly Ile Val Ala Gly Met Pro Ala Asn Asn Trp Thr Arg Leu Met
210 215 220

Ala Gly Asp Leu Asp Ala Ile Leu Ala Val Ser Val Asp Pro Ala Ser
225 230 235 240

His Leu Pro Val Ser Ala Leu Gly Leu Leu Tyr Arg Ser Val Leu Ala
245 250 255

Ala Cys Asp Gly Ile Asp Gly Val Val Asp Gly Val Leu Glu Asp Pro
260 265 270

Arg Arg Cys Arg Phe Asp Pro Ala Val Leu Met Cys Lys Ala Asp Gln
275 280 285

Asn Pro Asp Gly Cys Leu Thr Pro Ala Gln Val Glu Ala Ala Arg Arg
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Ile Tyr Gly Gly Leu Lys Asp Pro Lys Thr Gly Ala Gln Leu Tyr Pro
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Gly Leu Ala Pro Gly Ser Glu Pro Phe Trp Pro His Arg Asn Pro Ala
325 330 335

Asn Pro Phe Pro Ile Pro Ile Ala His Tyr Lys Trp Leu Val Phe Ala
340 345 350

Asp Pr